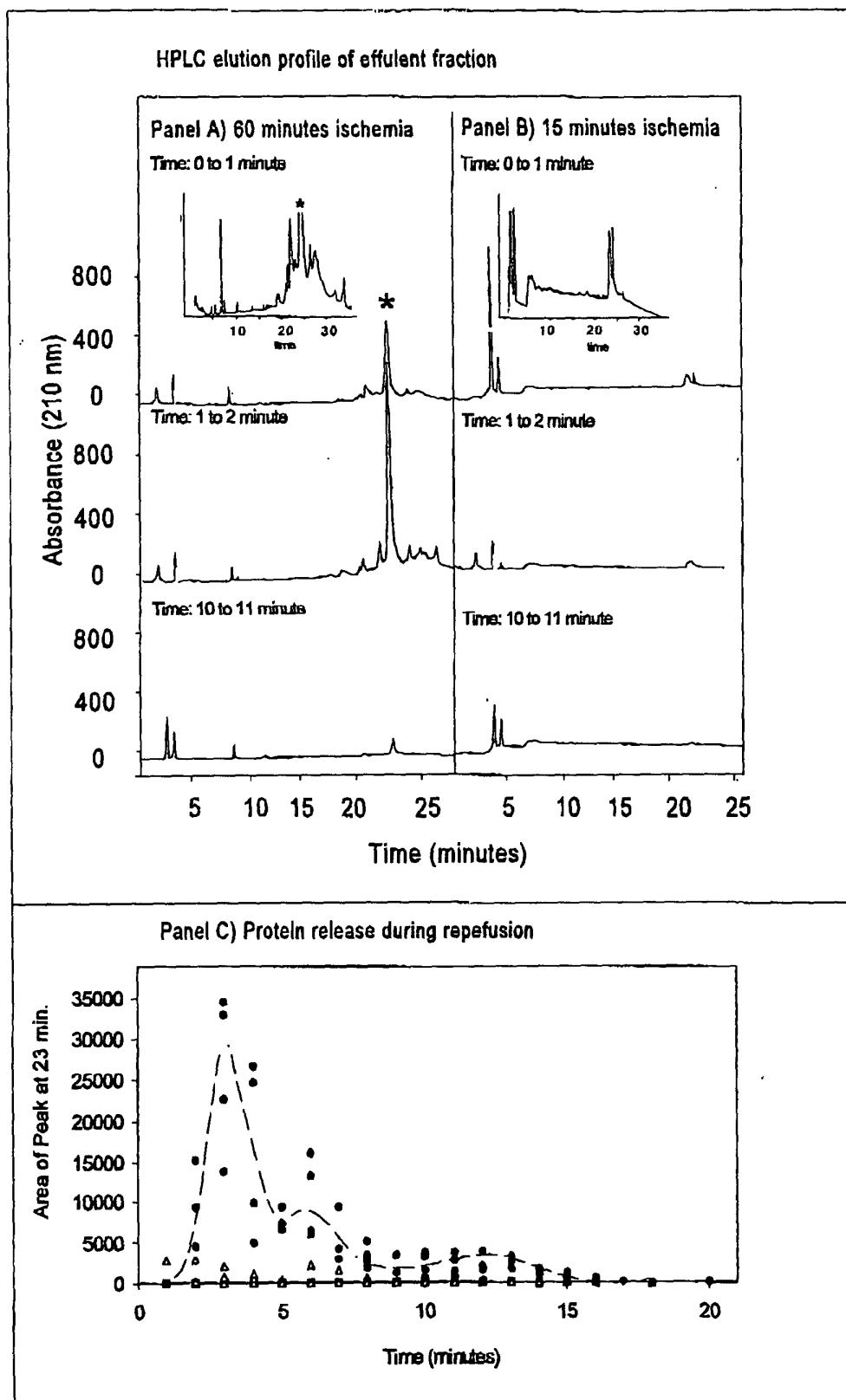
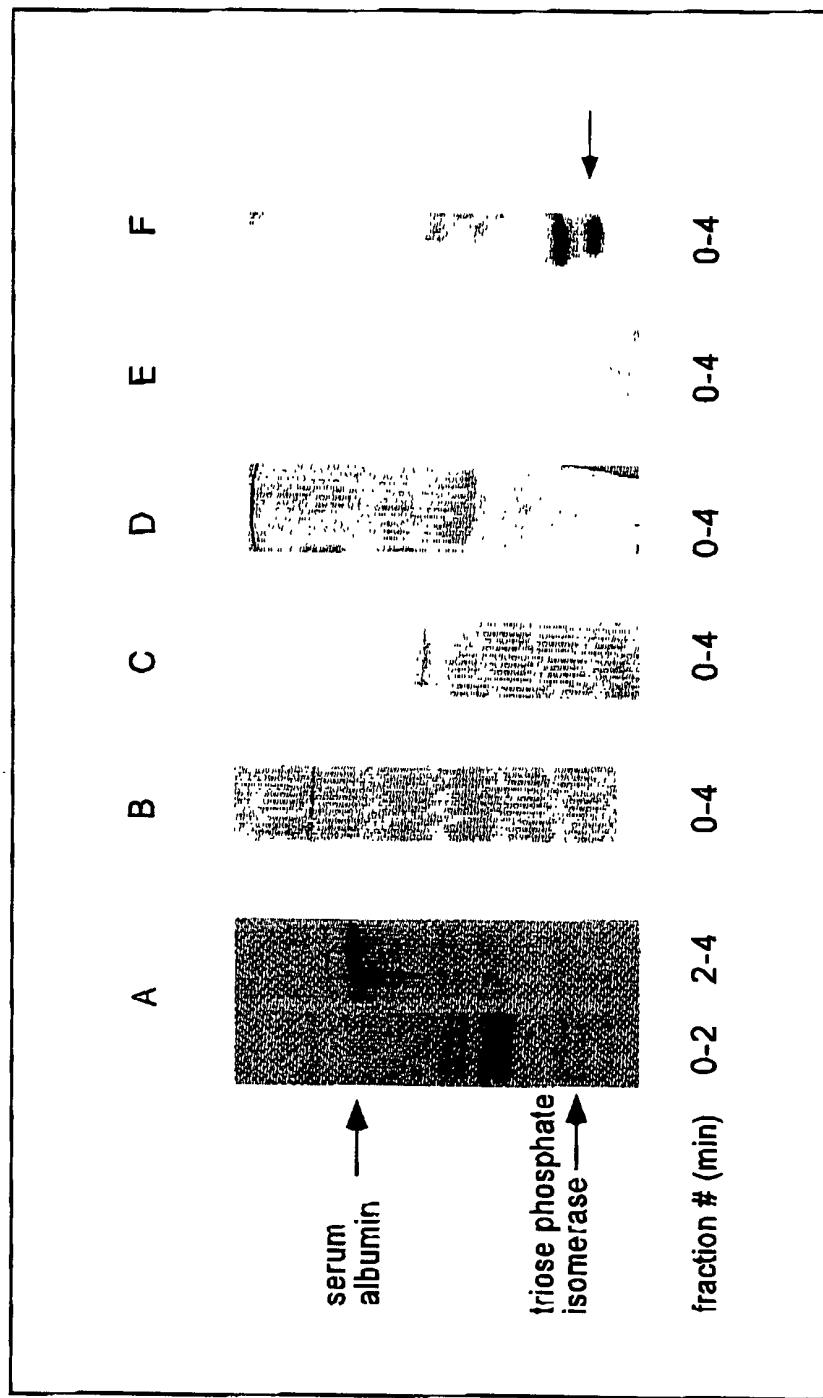


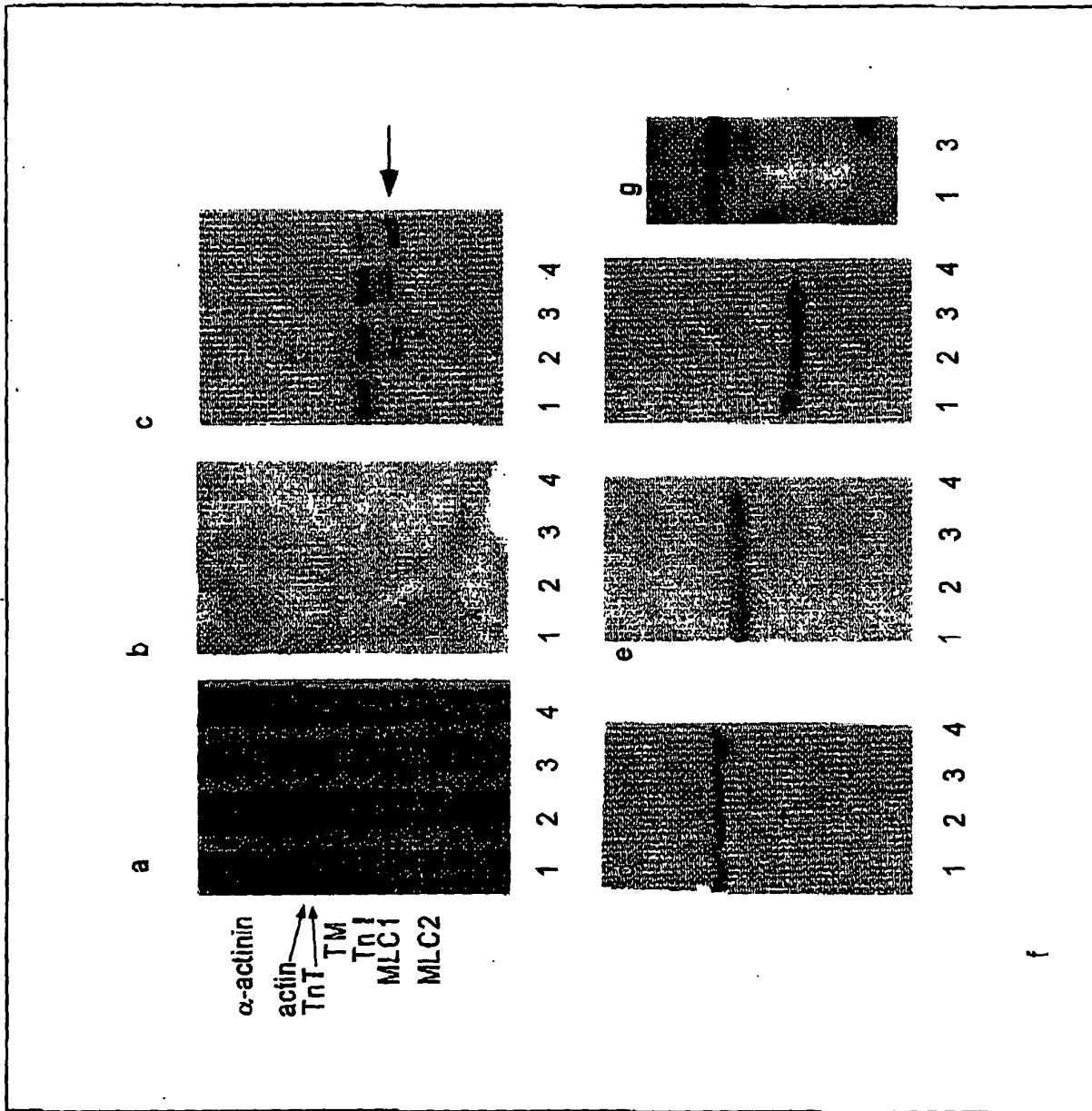
FIGURE 1

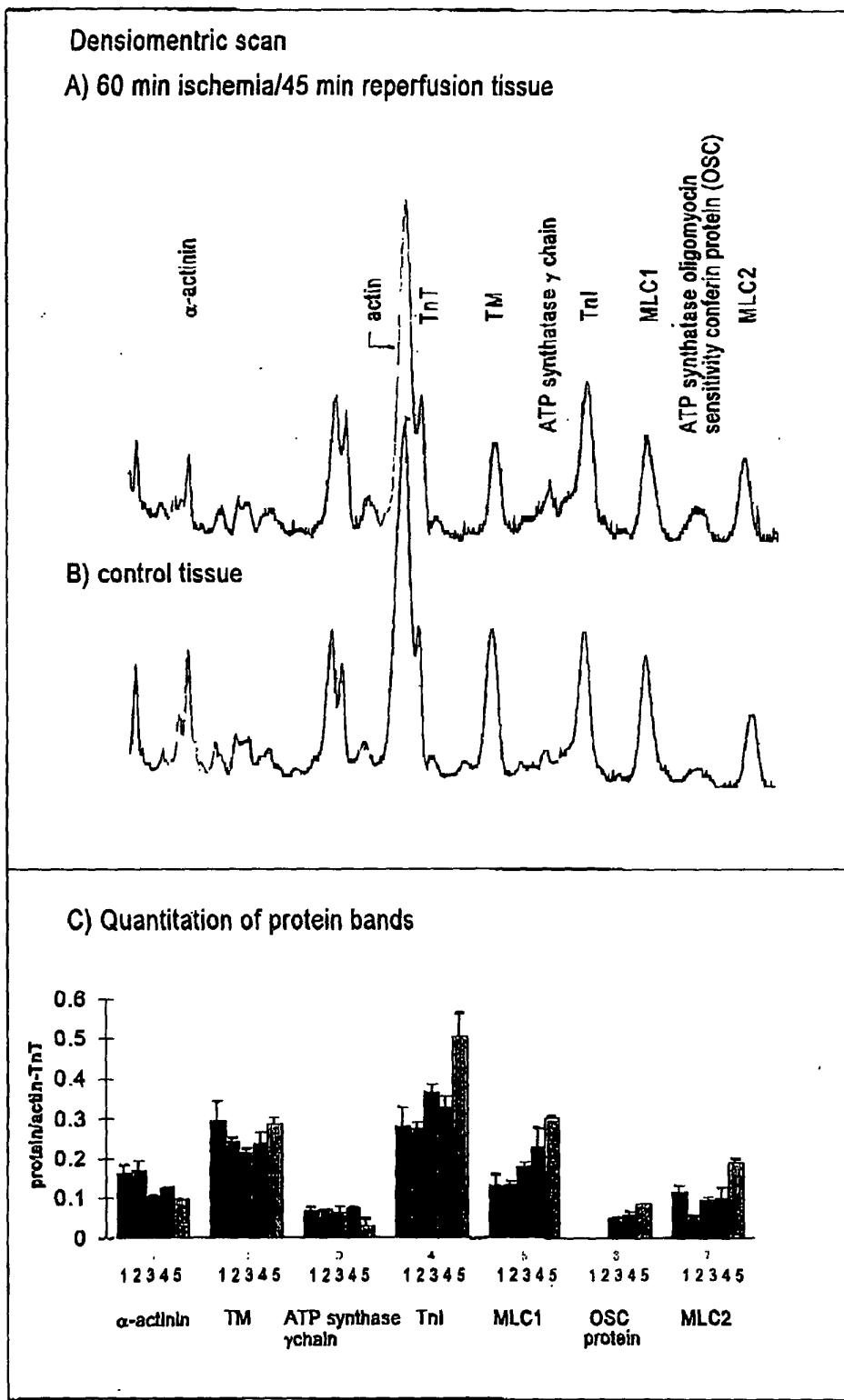
**FIGURE 2**



**FIGURE 3**

FIGURE 4



**FIGURE 5**

07/15/98 WED 15:46 FAX 545 6853 PARTEQ

007/022

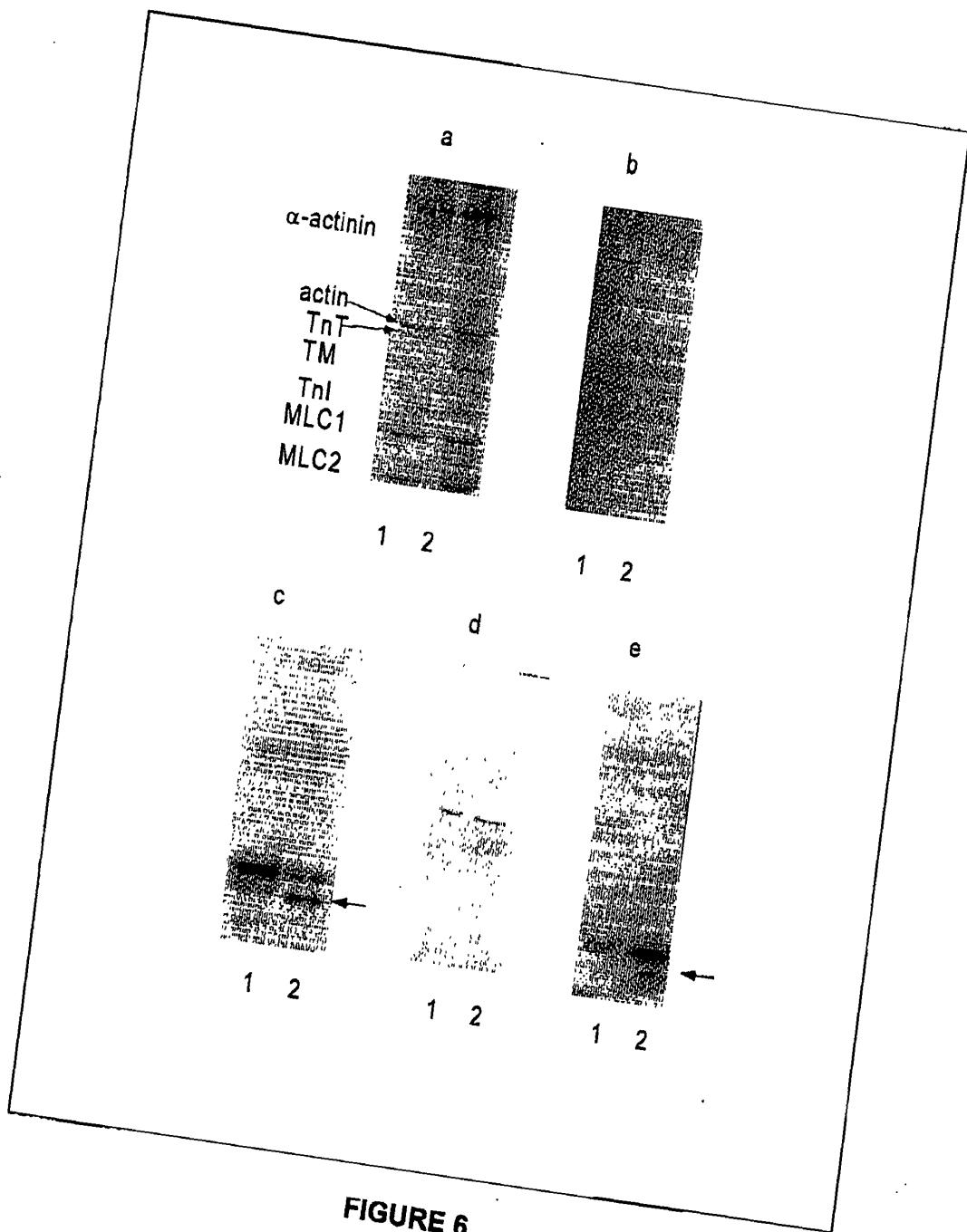
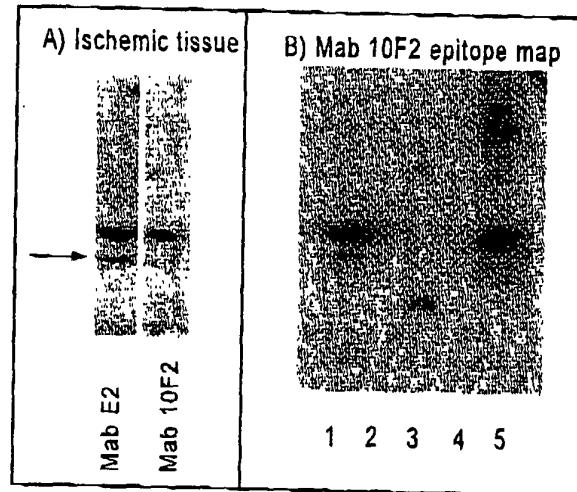
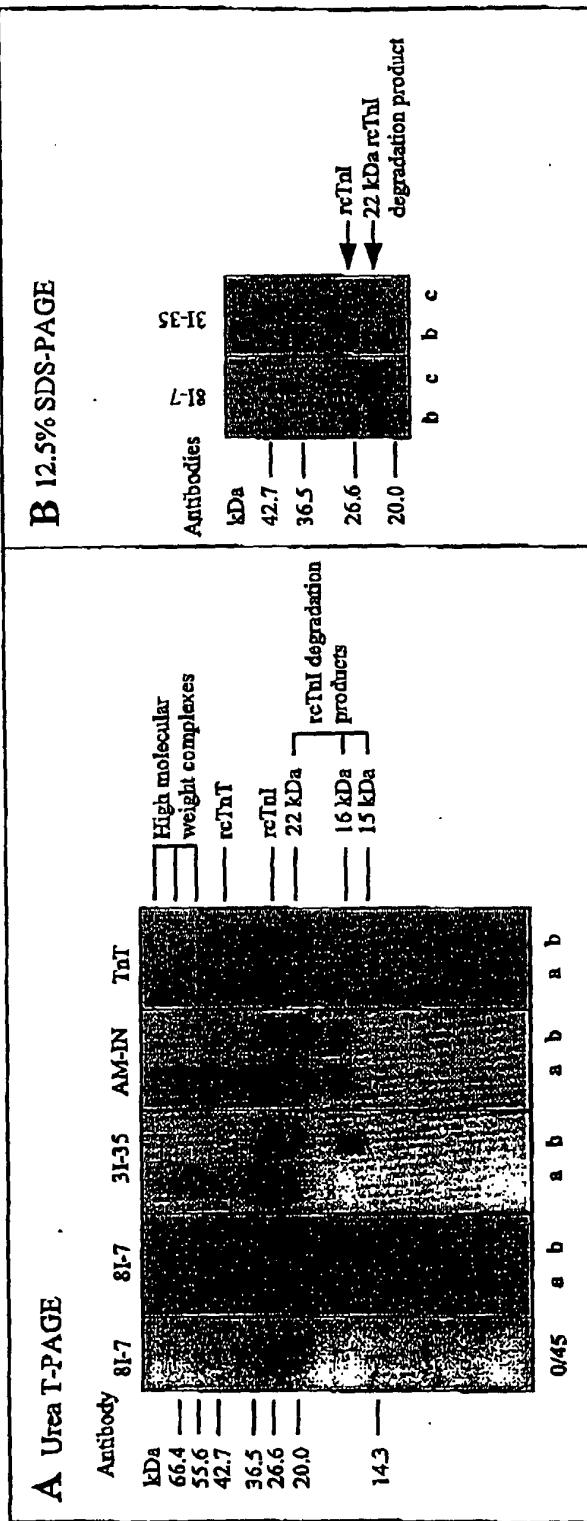


FIGURE 6

07/15 '98 16:55



**FIGURE 7**

**FIGURE 8**

**FIGURE 9**

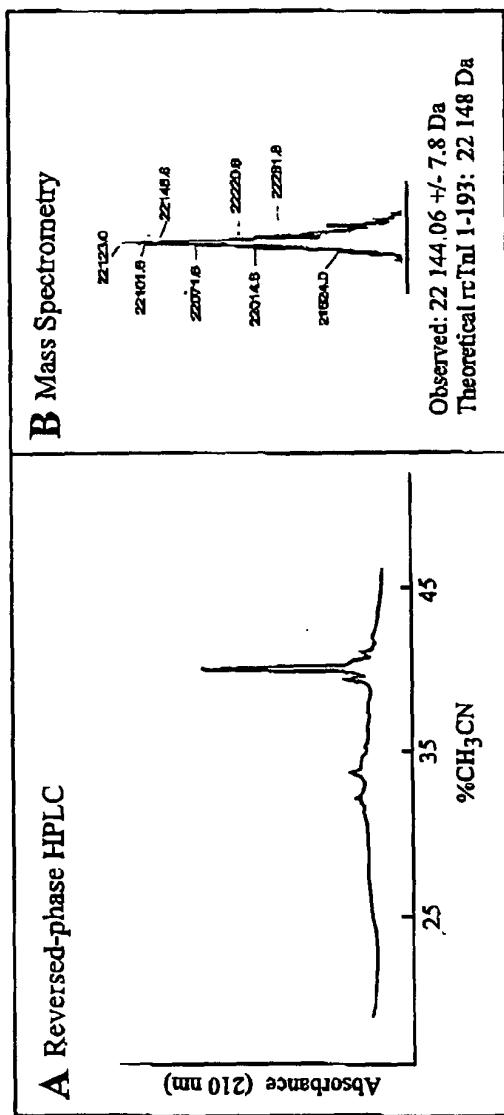
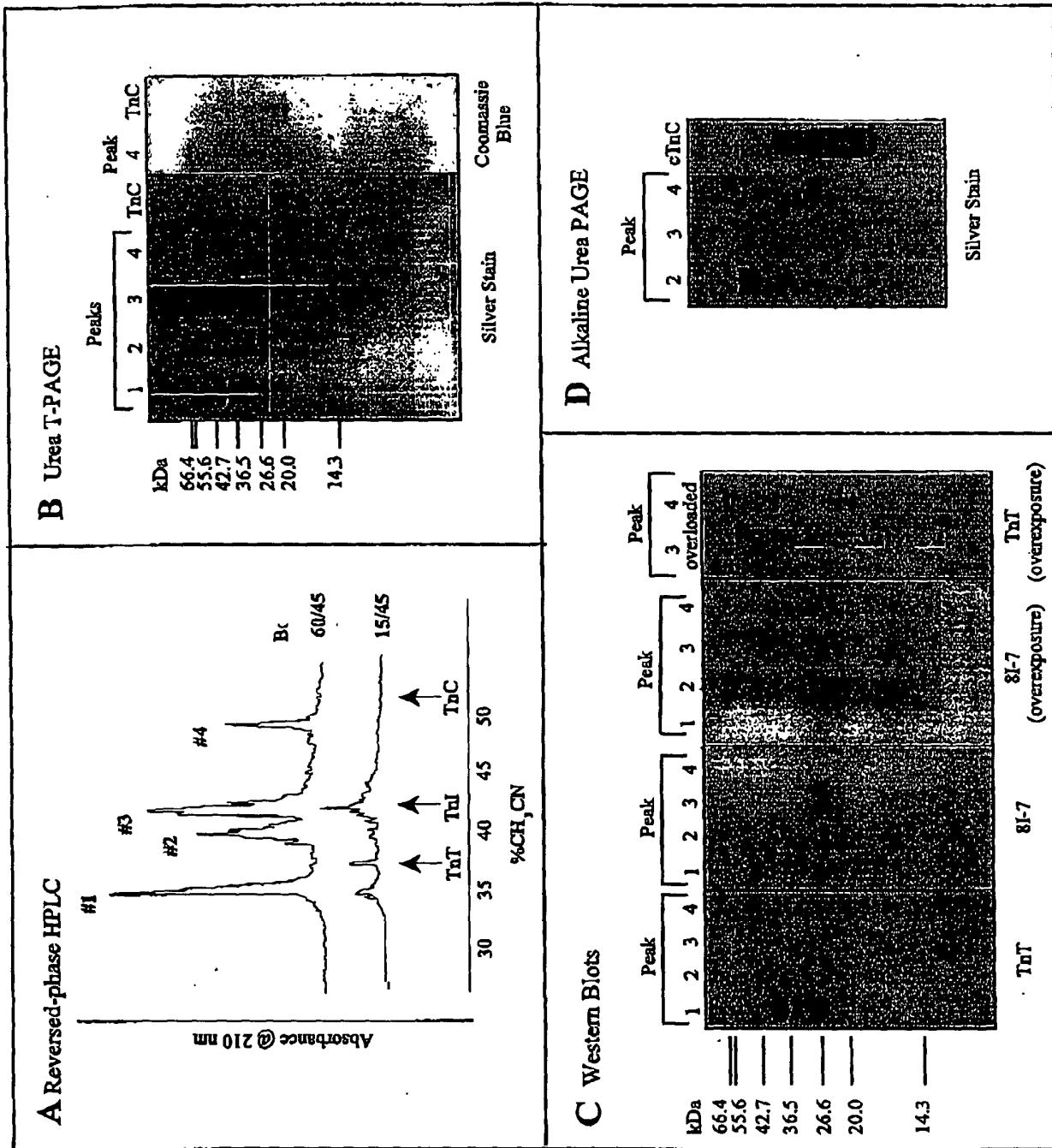
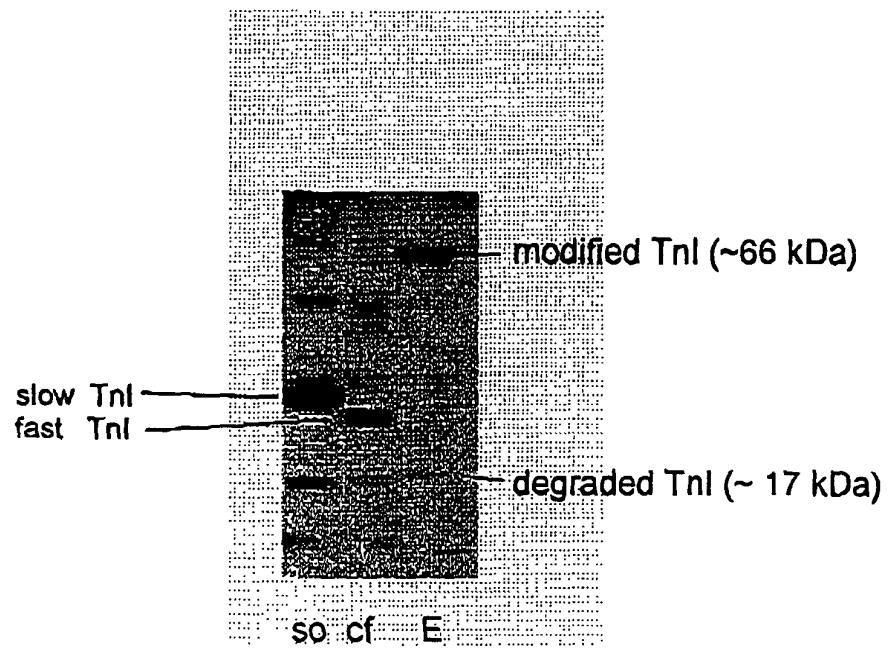
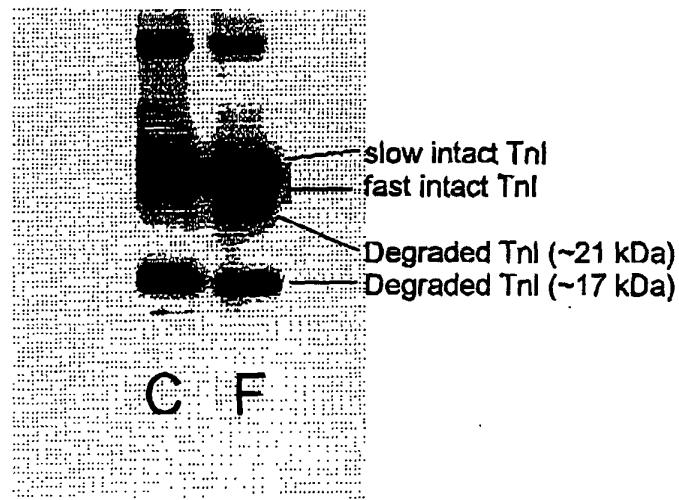


FIGURE 10



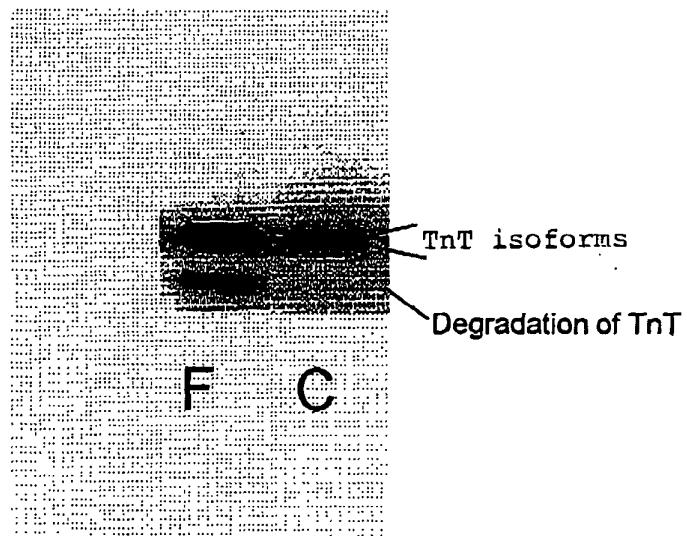


**FIGURE 11**



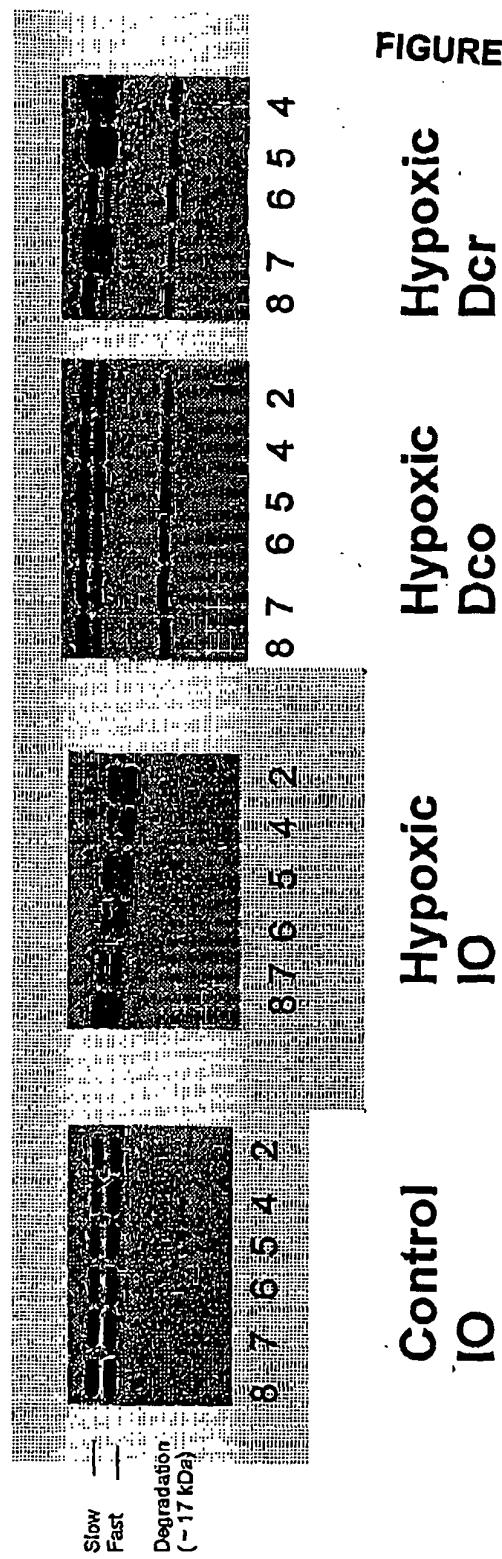
**FIGURE 12A**

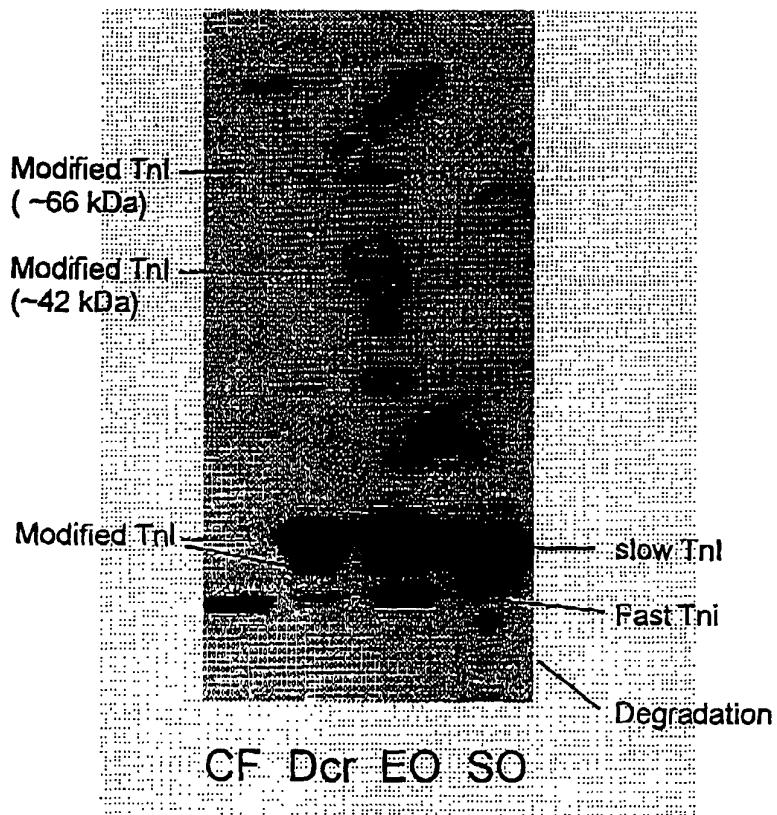
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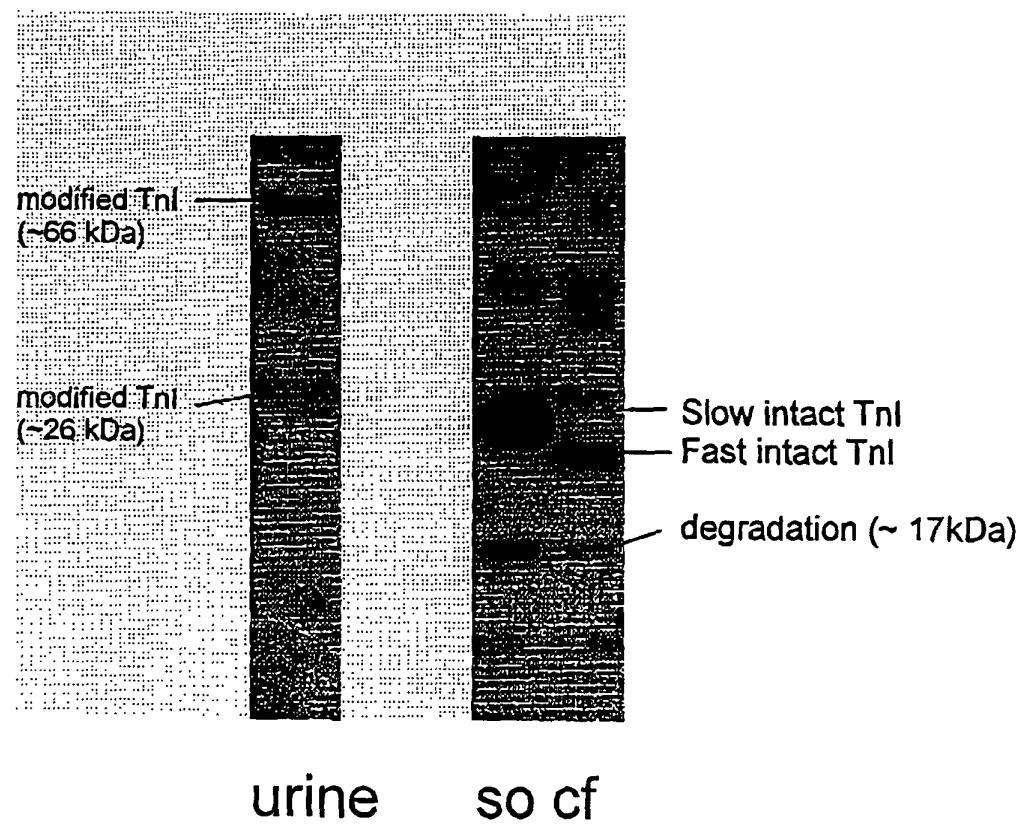
**FIGURE 12B**

FIGURE 13A





**FIGURE 13B**



**FIGURE 14**

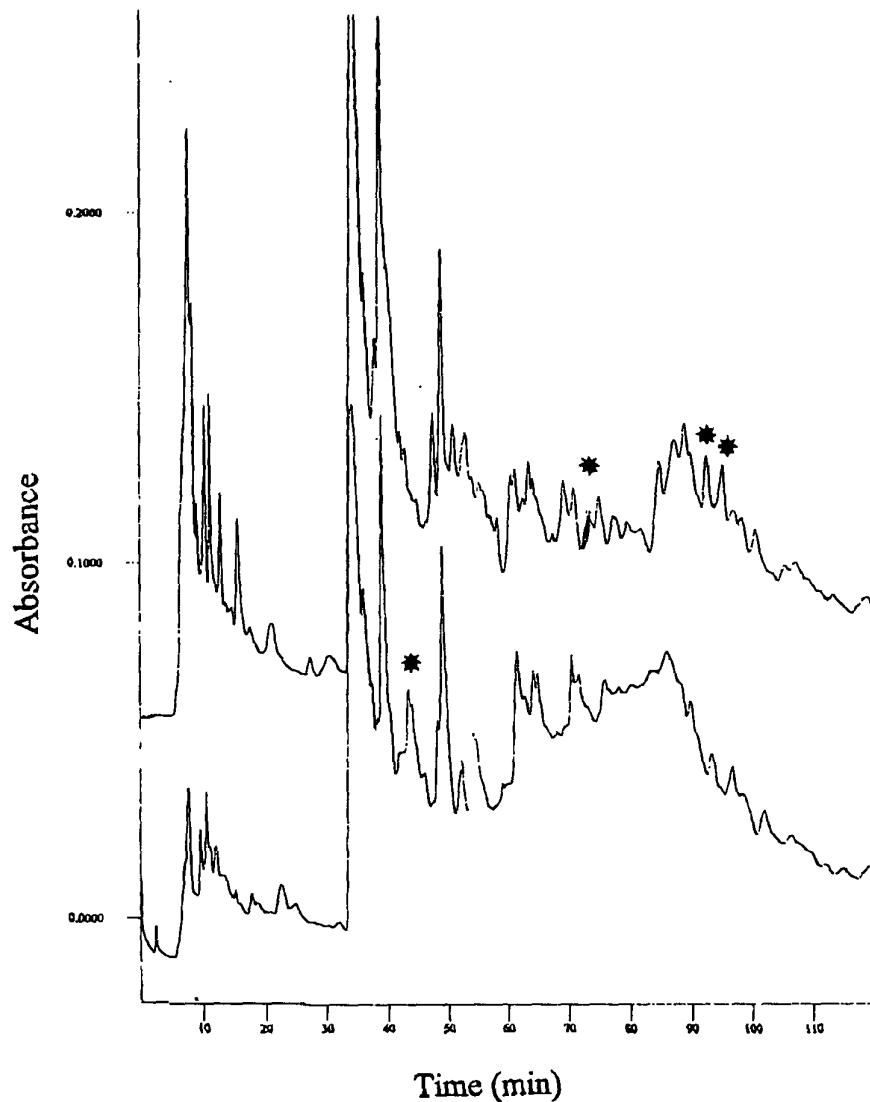
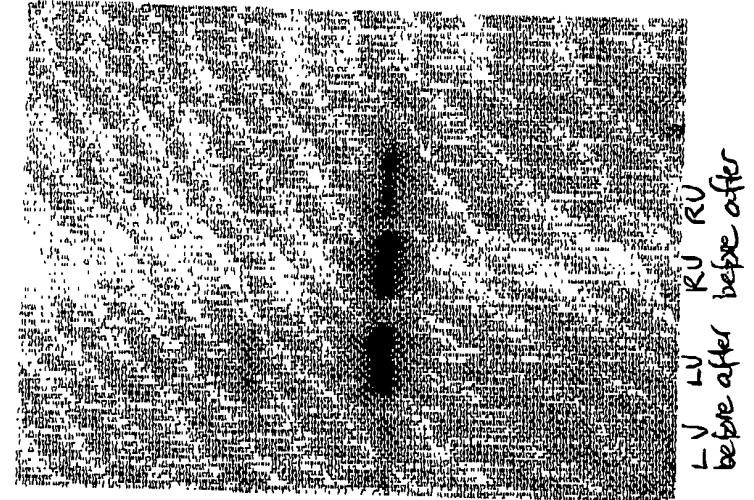
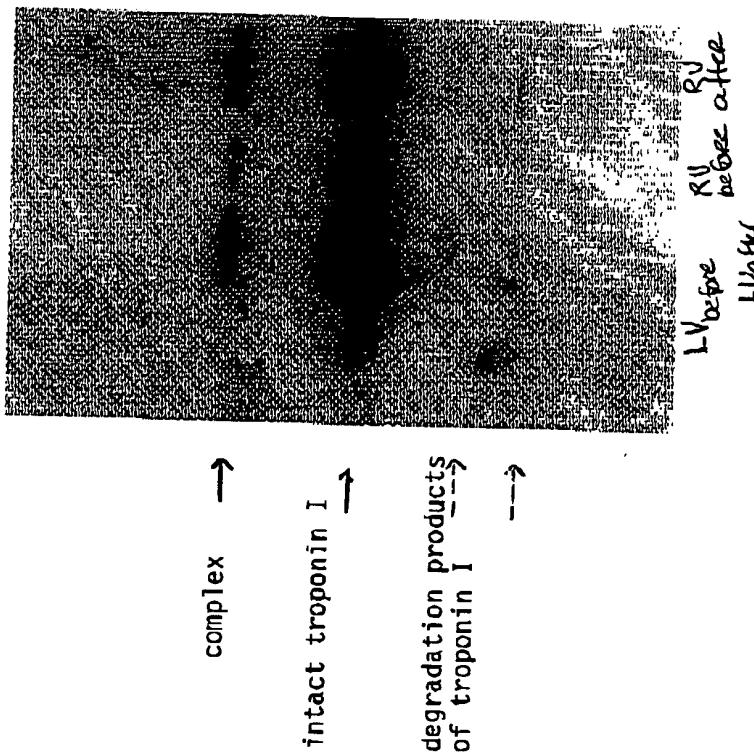
**FIGURE 15**

Figure . . HPLC analysis of normoxic (bottom trace ) and hypoxic urine (top trace) displayed at 278 nm. Some differences are noted with an asterisk. Each peak represents one or more proteins. The proteins were eluted with a 20 min isocratic wash (100 %A) followed by a linear gradient to 110 min (72% A; 28 % B) followed by another linear gradient to 120 min (20 % A; 80 %B). A-0.05% TFA in HOH; B-0.05% TFA in Acetonitrile.

FIGURE 16

Patient #1  
Patient #2



*Human Troponin I*

<b>cardiac</b>	ADGSSDAARE PRPAPAPIRR RSSNYRAYAT EPHAKKKSKI SASRKLQLKT
<b>slow skeletal</b>	..... .... .....
<b>fast skeletal</b>	..... .... .....
<b>cardiac</b>	LLLQIAKQEL EREAEERRGE KGRALSTRCQ PLELAGLGFA ELQDLCRQLH
<b>slow skeletal</b>	LMLAKAKECW EQEHEEREAE KVRYLAERIP TLQTRGLSLS ALQDLCRELH
<b>fast skeletal</b>	VMLQIAATEL EKEESRREAE KQNYLAEHCP PLHIPG.SMS EVQELCKOLH
<b>cardiac</b>	ARVDVKVDEER YDIEAKVTKN ITEIADLTQK IFDLRGKFKR PTLLRRVRISA
<b>slow skeletal</b>	AKVEVVDEER YDIEAKCLHN TREIKDLKLK VMDLRGKFKR PPRLRRVRVSA
<b>fast skeletal</b>	AKIDAAEEEK YDMEVRVQKT SKELEDMNQK LPDLRGKFKR PPRLRRVRMSA
<b>cardiac</b>	DAMMQALLGA RAKESLDLRA HLKQVKKEDT EKEN...REV GDWRKNIDAL
<b>slow skeletal</b>	DAMLALLGS KHKVSMDLRA NLKSVVKKEDT EKER..PVEV GDWRKNVEAM
<b>fast skeletal</b>	DAMLKALLGS KHKVCMDLRA NLKQVKKEDT EKERDL.RDV GDWRKNIEEK
<b>cardiac</b>	SGMEGRKKKF ES.....
<b>slow skeletal</b>	SGMEGRKKMF DAAKSPTSQ
<b>fast skeletal</b>	SGMEGRKKMF ESES....

1. Cardiac.....209 amino acids.....(P19429 - swiss prot identification number)  
VALLINS W.J., *et. al.*  
*FEBS LETT.* 270:57-61, 1990.
2. slow.....186 amino acids....(P19237 - swiss prot identification number)  
WADE R., *et. al.*  
*GENOMICS* 7:346-357, 1990.
3. fast.....181 amino acids....(P48788 - swiss prot identification number)  
ZHU L., *et. al.*  
*BIOCHIM. BIOPHYS. ACTA* 1217:338-340, 1994.

Sequences (1:2) Aligned. Score: 60  
 Sequences (1:3) Aligned. Score: 54  
 Sequences (2:3) Aligned. Score: 56

**FIGURE 17A**

**Rat Troponin I**

Human Cardiac	ADGSSDAARE PRPAPAPIRR RS.SNYRAYA TEPHAKKKSK ISASRKQLK
Rat Cardiac	ADESSDAAGE PQPAPAPVRR RSSANYRAYA TEPHAKKKSK ISASRKQLK
Rat Slow	..... . . . . . PEVERKSK ITASRKLMLK
Rat Fast	..... . . . . . GDEEKRNR AITARRQHLK
Human Cardiac	TLLLQIAKQE LEREAEERRG EKGRALSTRC QPLELAGLGF AELQDLCRQL
Rat Cardiac	TLMQIAKQE MERAEAEERRG EKGRVLSTRC QPLVLDGLGF EELQDLCRQL
Rat Slow	SLMLAKAKEC WEQEHEEREA EKVRYLSERI PTLQTRGLSL SALQDLCREL
Rat Fast	SVMLQIAATE LEKEESRRES EKQNYLSEHC PPLHIPGS.M SEVQELCKQL
Human Cardiac	HARVDKVDEE RYDIEAKVTK NITEIADLTQ KIFDLRGKFK RPTLRRVRIS
Rat Cardiac	HARVDKVDEE RYDVEAKVTK NITEIADLTQ KIYDLRGKFK RPTLRRVRIS
Rat Slow	HAKVEVVDDEE RYDIEAKCLH NTREIKDLKL KVLDLRGKFK RPPPLRRVRVS
Rat Fast	HAKIDAAEEE KYDMEVKVQK SSKELEDMNQ KLFDLRGKFK RPPLRRVRMS
Human Cardiac	ADAMMQALLG ARAKESLDLR AHLKQVKKED TEKEN...RE VGDWRKNIDA
Rat Cardiac	ADAMMQALLG TRAKESLDLR AHLKQVKKED IEKEN...RE VGDWRKNIDA
Rat Slow	ADAMLRALLG SKHKVSMDLR ANLKSVKKKED TEKER..PVE VGDWRKNVEA
Rat Fast	ADAMLKALLG SKHKVCMDLR ANLKQVKKED TEKERDL.RD VGDWRKNIEE
Human Cardiac	LSGMEGRKKK FES.....
Rat Cardiac	LSGMEGRKKK FEG.....
Rat Slow	MSGMGRKKM FDAAKSPTLQ
Rat Fast	KSGMGRKKM FESES.....

1. Human cardiac TnI....209 amino acids ( P19429 - swiss prot identification number)  
VALLINS W.J., *et. al.*  
*FEBS LETT.* 270:57-61,1990.
2. Rat Cardiac TnI.....210 amino acids ( P23693 - swiss prot identification number)  
MURPHY A.M., *et al.*  
*BIOCHEMISTRY* 30:707-712, 1991.
3. Rat slow TnI.....186 amino acids ( P13413 - swiss prot identification number)  
KOPPE R.I., *et. al.*  
*J. BIOL. CHEM.* 264:14327-14333, 1989.
4. Rat fast TnI.....181 amino acids ( P27768 - swiss prot identification number)  
GRAVEL M., HASTINGS K.E.;  
SUBMITTED (XXX-1991) TO EMBL/GENBANK/DDBJ DATA BANKS.

Sequences (1:2) Aligned. Score: 92  
 Sequences (1:3) Aligned. Score: 61  
 Sequences (1:4) Aligned. Score: 55  
 Sequences (2:3) Aligned. Score: 60  
 Sequences (2:4) Aligned. Score: 54  
 Sequences (3:4) Aligned. Score: 56

**FIGURE 17B**

*Human Troponin T*

Cardiac	SDIEEVVEBY RBBBQEEAAV EEQEEAAEED AEEAEETEET RAAEDEEEEEE
Slow skeletal	SDTEE..QEY EEEQPBBBBAA EE.....EEE APPE..PEP. VAE.....
fast skeletal	SD.EE.VEQV EEQYEEEEAA QE.....EEE VQED..TAEE DAE.....
Cardiac	AKEAEDGPME ESKPKP.RSF MPNLVPPKIP DGERVDFDDI HRKRMEKDLM
Slow skeletal	.....PEE E.RPKPSRPV VPPLIPPKIP EGERVDFDDI HRKRMEKDLM
fast skeletal	.....EE K..PRP.... .KLTAPKIP EGEKVDVFDDI QKKRQNKDLM
Cardiac	ELQALIEAHF ENRKKEEEEL VSLKDRIERR RAERAEQQRI RNEREKERQN
Slow skeletal	ELQTLIDVHF EQRKKEEEEL VALKERIERR RSERAEQQRF RTEKERERQA
fast skeletal	ELQALIDSHF EARKKEEEEL VALKERIEKR RAERAEQQRI RAEKERERQN
Cardiac	RLAEEERARRE EENNRKAED EARKKKALSN M.MHFGGYIQ KQAQTERKSG
Slow skeletal	KLAEEKMRKE EEEAKKRAED DAKKKKVLSN MGAHFGGYLV KAEQK.R..G
fast skeletal	RLAEEKARRE EEDAKKRAED DLKKKKALSS MGANYSSYLA KADQK.R..G
Cardiac	KRQTEREBKKK KILAERRKVL AIDHLNEDQL R..... EKA
Slow skeletal	KRQTGREMKV RILSERKKPL DIDYMGEQL RARSawlPPS QPSCPAREKA
fast skeletal	KKQTAREMKK KILAERRKPL NIDHGEDKL R..... DKA
Cardiac	KELWQSIYNL EAEKFDLQEK FKQQKYEINV LRNRINDNQK VSCTR...K
Slow skeletal	QELSDWIHQL ESEKFDLMAK LKQQKYEINV LYNRISHAQK FRKGAG...K
fast skeletal	KELWETLHQL EIDKFEGEKG LKRQKYDITT LRSRIDQAQK HSKKAGTPAK
Cardiac	AKVTGRWK
Slow skeletal	GRVGGGRWK
fast skeletal	GKVGGGRWK

**Consensus length = 308**

1. Cardiac.....287 amino acids....(P45379 - swiss prot identification number)

MESNARD L., *et. al.*

*FEBS LETT.* 328:139-144, 1993.

2. slow.....277 amino acids....(P13805 - swiss prot identification number)

GAHLMANN R., *et. al.*

*J. BIOL. CHEM.* 262:16122-16126, 1987.

3. fast.....257 amino acids....(P45378 - swiss prot identification number)

WU Q.-L., *et. al.*

*DNA CELL BIOL.* 13:217-233, 1994.

Sequences (1:2) Aligned. Score: 58

Sequences (1:3) Aligned. Score: 61

Sequences (2:3) Aligned. Score: 63

**FIGURE 17C**

## Rat Troponin T

Human Cardiac	SDIEEVVVEEY EEEEQEE... . . . . . AA VEEQEEAAEE DAEAEAETEE
Rat Cardiac	SDAEEEVVEY EEEQEEEDWS EEEEDEQEEA VEEEDGEAEP DPEGEAEAEE
Rat Fast sk	. SDEETEQV EEQYEEE... . . . . . E E. . . . . AQ. . . . . EEE
Human Cardiac	TRAEEDEEEE EAKEAEDGPM EESKPKP.RS FMPNLVPPKI PDGERVDFDD
Rat Cardiac	DKAEEVGPD EARDAAEDGPV EDSKPKPSRL FMPNLVPPKI PDGERVDFDD
Rat Fast sk	. VQEEAPEPE EVQEEE. . . . . KPRP. . . . . KLTAPKI PEGEKVDFDD
Human Cardiac	IHRKRMEKDL NELQALIEAH FENRKKEEEE LVSLKDRIER RRAERAEQQR
Rat Cardiac	IHRKRMEKDL NELQTLIEAH FENRKKEEEE LISLKDRIEK RRAERAEQQR
Rat Fast sk	IQKKRQNKL MELQALIDSH FEARKKEEEE LIALKERIEK RRAERAEQQR
Human Cardiac	IRNERECKERQ NRLAEEARR EEEENRRKAE DEARKKKALS NMMHFGGYIQ
Rat Cardiac	IRNERECKERQ NRLAEEARR EEEENRRKAE DEARKKKALS NMMHFGGYIQ
Rat Fast sk	IRAEKERERQ NRLAEEKARR EEEADAKRAE DDLKKKKALS SMG.. ANYSS
Human Cardiac	KQAQTERKSG KRQTEREKKK KILAERRKVL AIDHLNEDQL REKAKELWQS
Rat Cardiac	K. AQTERKSG KRQTEREKKK KILAERRKVL AIDHLNEDQL REKAKELWQS
Rat Fast sk	YLAKADQKRG KKQTAREMKK KILAERRKPL NIDHLSDDKL RDKAKEWLDT
Human Cardiac	IYNLEAEKFD LQEKFQKQKY EINVLRNRIN DNQKVSKTRG . . . KAKVTGR
Rat Cardiac	IHNLEAEKFD LQEKFQKQKY EINVLRNRIN DNQKVSKTRG . . . KAKVTGR
Rat Fast sk	LYQLETDKFE FGEEKLKRQKY DITTLRSRID QAQKHSKKAG ATAKGVGGR
Human Cardiac	WK
Rat Cardiac	WK
Rat Fast sk	WK

1. Human cardiac TnT....287 amino acids ( P45379 - swiss prot identification number)

MESNARD L., et. al.

*FEBS LETT.* 328:139-144, 1993.

2. Rat Cardiac TnT.....298 amino acids ( P50753 - swiss prot identification number)

JIN J.-P., et. al.

*J. BIOL. CHEM.* 264:14471-14477, 1989.

3. Rat fast TnT.....258 amino acids ( P09739 - swiss prot identification number)

BREITBART R.E., et. al.

*J. MOL. BIOL.* 188:313-324, 1986.

Sequences (1:2) Aligned. Score: 88

Sequences (1:3) Aligned. Score: 60

Sequences (2:3) Aligned. Score: 59

Consensus length = 302

## FIGURE 17D